AMENDMENT TO THE CLAIMS

1. **(Original)** A method of identifying a binding site domain having the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bi- or multivalent polypeptide comprising the steps of

   (a) testing a panel of binding site domains displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, wherein said fusion protein comprises an additional domain positioned N-terminal of said binding site domain and an amino acid sequence that mediates anchoring of the fusion protein to the surface of said display system; and

   (b) identifying a binding site domain that binds to said predetermined epitope.

2. **(Original)** The method of claim 1, wherein said binding site domain and said additional domain are linked by a polypeptide linker disposed between said binding site and said additional domain, wherein said polypeptide linker comprises plural, hydrophilic, peptide-bonded amino acids and connects the N-terminal end of said binding site domain and the C-terminal end of said additional domain.

3. **(Original)** The method of claim 1 or 2, wherein said binding site domain is a pair of V_H-V_L, V_H-V_H or V_L-V_L domains.

4. **(Previously Presented)** The method of claim 1 wherein said display system is a filamentous phage produced by bacteria transfected therewith, a baculovirus expression system, a ribosome based expression system, a bacteriophage lambda display system or a bacterial surface expression system.

5. **(Original)** The method of claim 4 comprising, prior to step (a), the further step of

   (a") transfecting bacteria with recombinant vectors encoding said fusion proteins.

6. **(Previously Presented)** The method of claim 1 comprising, prior to step (a"), the further step of

(a') cloning a panel of nucleic acid molecules encoding said binding site domains into a vector.

7. **(Original)** The method of claim 6, wherein said panel of nucleic acid molecules is derived from immune competent cells of a mammal, fish or bird.

8. **(Previously Presented)** The method of claim 1, wherein said additional domain comprises at least 9 amino acids.

9. **(Original)** The method of claim 8, wherein said additional domain is or is derived from the N2-domain of the gene III product of filamentous phage.

10. **(Previously Presented)** The method of claim 1, wherein said sequence that mediates said anchoring is or is derived from the C-terminal CT-domain of the gene III product of filamentous phage.

11. **(Previously Presented)** The method of claim 1, wherein said bi- or multivalent polypeptide is a bi- or multifunctional polypeptide.

12. **(Original)** The method of claim 9, wherein said at least one further domain comprises polypeptide selected from the group consisting of effector proteins having a conformation suitable for biological activity, amino acid sequences capable of sequestering an ion, and amino acid sequences capable of selective binding to a solid support.

13. **(Original)** The method of claim 12 wherein said effector protein is an enzyme, toxin, receptor, binding site, biosynthetic antibody binding site, growth factor, cell-differentiation factor, lymphokine, cytokine, hormone, a remotely detectable moiety, or anti-metabolite.

14. **(Original)** The method of claim 12 wherein said sequence capable of sequestering an ion is calmodulin, methallothionein, a fragment thereof, or an amino acid sequence rich in at least one of glutamic acid, aspartic acid, lysine, and arginine.

15. **(Original)** The method of claim 12 wherein said polypeptide sequence capable of selective binding to a solid support is a positively or negatively charged amino acid sequence, a cysteine-containing amino acid sequence, streptavidin, or a fragment of Staphylococcus protein A.

16. **(Original)** The method of claim 13, wherein said receptor is a co-stimulatory surface molecule important for T-cell activation or comprises an epitope binding site or a hormone binding site.

17. **(Original)** The method of claim 16, wherein said co-stimulatory surface molecule is CD80 (B7-1), CD86 (B7-2), CD58 (LFA-3) or CD54 (ICAM-1).

18. **(Original)** The method of claim 17, wherein said epitope binding site is embedded in a pair of V_H-V_L, V_H-V_H or V_L-V_L domains.

19. **(Previously Presented)** The method of claim 3, wherein said pair of domains are connected by a flexible linker, preferably by a polypeptide linker disposed between said domains, wherein said polypeptide linker comprises plural, hydrophilic, peptide-bonded amino acids of a length sufficient to span the distance between the C-terminal end of one of said domains and the N-terminal end of the other of said domains when said fusion protein assumes a conformation suitable for binding when disposed in aqueous solution.

20. **(Previously Presented)** The method of claim 1, wherein the identification of said binding site domain comprises the steps of

(b') removing said amino acid sequence that mediates anchoring of the fusion protein to the surface of a phage from said fusion protein;

(b") periplasmatically expressing the nucleic acid molecules encoding the remainder of said fusion protein in bacteria; and

(b"') verifying whether said binding site domain binds to said predetermined epitope.

21. **(Original)** Kit comprising

(a) a panel of recombinant vectors encoding a panel of fusion proteins as defined in any one of claims 1 to 20; and/or

(b) a bacterial library transfected with a panel of vectors as defined in (a).

22. **(Previously Presented)** A binding site domain or fusion protein obtainable by the method of claim 1, wherein said binding site domain comprises at least one complementarity determining region (CDR) of the scFv fragment shown in any one of figures 6.3 to 6.10 and 7.

23. **(Original)** A polypeptide or an antibody comprising at least one binding site domain or fusion protein of claim 22.

24. **(Original)** The polypeptide or antibody of claim 23 having the amino acid sequence as depicted in any one of figures 6.3 to 6.10 and 7.

25. **(Original)** Polynucleotides which upon expression encode the polypeptide or antibody of claim 23 or 24.

26. **(Original)** A cell transfected with a polynucleotide of claim 25.

27. **(Original)** A process for the preparation of a polypeptide or antibody of claim 23 or 24 comprising cultivating a cell of claim 26 under conditions suitable for the expression of the polypeptide and isolating the polypeptide from the cell culture medium.

28. **(Original)** A pharmaceutical composition containing a polypeptide or antibody of claim 23 or 24 and optionally a pharmaceutically acceptable carrier.

29. **(Original)** A diagnostic composition comprising the polypeptide or antibody of claim 23 or 24 and optionally suitable means for detection.

30. **(New)** A binding site domain or fusion protein obtainable by the method of claim 1, wherein said binding site domain or fusion protein comprises at least one complementary determining region (CDR) of the scFv fragment shown in figure 6.10.

31. **(New)** A polypeptide or an antibody comprising at least one binding site domain or fusion protein of claim 30.

32. **(New)** The polypeptide or antibody of claim 23, having the amino acid sequence as depicted in figure 6.10.

33. **(New)** The polypeptide of claim 32 having the amino acid sequence according to SEQ ID No. 75.